

SEQUENCE LISTING

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Collier, Robert J.
Mogridge, Jeremy S.

<120> Anthrax Toxin Receptor

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<150> 60/251,481

<151> 2000-12-05

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<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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Met Ala Thr Ala
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gag cgg aga gcc ctc ggc atc ggc ttc cag tgg ctc tct ttg gcc act 163
Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr
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ctg gtg ctc atc tgc gcc ggg caa ggg gga cgc agg gag gat ggg ggt 211
Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly
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cca gcc tgc tac ggc gga ttt gac ctg tac ttc att ttg gac aaa tca 259
Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser
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gga agt gtg ctg cac cac tgg aat gaa atc tat tac ttt gtg gaa cag 307
Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln
55 60 65

ttg gct cac aaa ttc atc agc cca cag ttg aga atg tcc ttt att gtt 355
Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met Ser Phe Ile Val
70 75 80

tct gtc atc atc acc acc aca cac tgt tct gac ggt tcc atc ctg gcc 1075
 Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly Ser Ile Leu Ala
 310 315 320

atc gcc ctg ctg atc ctg ttc ctg ctc cta gcc ctg gct ctc ctc tgg 1123
 Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu Ala Leu Leu Trp
 325 330 335 340

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 345 350 355

ccc cct gcc gag gag agt gag gaa aat aaa ata aaa taacaagaag 1217
 Pro Pro Ala Glu Glu Ser Glu Glu Asn Lys Ile Lys
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 35 40 45

Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
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Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
 65 70 75 80

Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
 85 90 95

Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
 100 105 110

Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
 115 120 125

Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
 130 135 140

Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
 145 150 155 160
 Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
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 Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
 180 185 190
 Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
 195 200 205
 Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
 210 215 220
 Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
 225 230 235 240
 Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
 245 250 255
 Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
 260 265 270
 Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
 275 280 285
 Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
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 Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly
 305 310 315 320
 Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu
 325 330 335
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<223> Description of Artificial Sequence: von Willebrand
factor A domain consensus sequence

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 35 40 45
 Ser Asp Ala Arg Val Leu Phe Pro Leu Asn Asp Ser Gln Ser Lys Asp
 50 55 60
 Ala Leu Leu Glu Ala Leu Ala Asn Leu Ser Tyr Ser Leu Gly Gly Gly
 65 70 75 80
 Thr Asn Leu Gly Ala Ala Leu Glu Tyr Ala Leu Glu Asn Leu Phe Ser
 85 90 95
 Glu Ser Ala Gly Ser Arg Arg Gly Ala Pro Lys Val Leu Ile Leu Ile
 100 105 110
 Thr Asp Gly Glu Ser Asn Asp Gly Gly Glu Asp Ile Leu Lys Ala Ala
 115 120 125
 Lys Glu Leu Lys Arg Ser Gly Val Lys Val Phe Val Val Gly Val Gly
 130 135 140
 Asn Ala Val Asp Glu Glu Glu Leu Lys Lys Leu Ala Ser Ala Pro Gly
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 Asp Leu Leu Leu
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 Ala Asn Asn Pro Arg Val Val Phe Asn Leu Asn Thr Tyr Lys Thr Lys
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 Glu Glu Met Ile Val Ala Thr Ser Gln Thr Ser Gln Tyr Gly Gly Asp
 65 70 75 80

Leu Thr Asn Thr Phe Gly Ala Ile Gln Tyr Ala Arg Lys Tyr Ala Tyr
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 100 105 110
 Val Thr Asp Gly Glu Ser His Asp Gly Ser Met Leu Lys Ala Val Ile
 115 120 125
 Asp Gln Cys Asn His Asp Asn Ile Leu Arg Phe Gly Ile Ala Val Leu
 130 135 140
 Gly Tyr Leu Asn Arg Asn Ala Leu Asp Thr Lys Asn Leu Ile Lys Glu
 145 150 155 160
 Ile Lys Ala Ile Ala Ser Ile Pro Thr Glu Arg Tyr Phe Phe Asn Val
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 Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr Leu Val Leu Ile Cys Ala
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 Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly
 30 35 40
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 Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His
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Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Lys Phe Ile	
60 65 70	
agc cca cag ttg aga atg tcc ttt att gtt ttc tcc acc cga gga aca	413
Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr	
75 80 85 90	
acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta	461
Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu	
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Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu	
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Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly	
125 130 135	
tac agg aca gcc agc gtc atc att gct ttg act gat gga gaa ctc cat	605
Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His	
140 145 150	
gaa gat ctc ttt ttc tat tca gag agg gag gct aat agg tct cga gat	653
Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp	
155 160 165 170	
ctt ggt gca att gtt tac tgt gtt ggt gtg aaa gat ttc aat gag aca	701
Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr	
175 180 185	
cag ctg gcc cgg att gcg gac agt aag gat cat gtg ttt ccc gtg aat	749
Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val Asn	
190 195 200	
gac ggc ttt cag gct ctg caa ggc atc atc cac tca att ttg aag aag	797
Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys	
205 210 215	
tcc tgc atc gaa att cta gca gct gaa cca tcc acc ata tgt gca gga	845
Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly	
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Glu Ser Phe Gln Val Val Val Arg Gly Asn Gly Phe Arg His Ala Arg	
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ctc aat gag aag ccc ttt tct gtg gaa gat act tat tta ctg tgt cca	989
Leu Asn Glu Lys Pro Phe Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro	
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Phe Leu Leu Leu Ala Leu Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys	
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Cys Thr Val Ile Ile Lys Glu Val Pro Pro Pro Pro Ala Glu Glu Ser	
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ccc ccg ccc ccc agc gcc cct acc cct ccc atc ccg tcc cca cct tcc 1757
 Pro Pro Pro Pro Ser Ala Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser
 525 530 535

acc ctt ccc cct cct ccc cag gct cca cct ccc aac agg gca cct cct 1805
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 540 545 550

ccc tcc cgc cct cct cca agg cct tct gtc tagagcccaa agttcctgct 1855
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Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
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Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
 65 70 75 80

Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
 85 90 95

Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
 100 105 110

Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
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Glu 130	Gln 130	Ile 130	Tyr 130	Tyr 130	Glu 135	Asn 135	Arg 135	Gln 135	Gly 135	Tyr 140	Arg 140	Thr 140	Ala 140	Ser 140	Val 140
Ile 145	Ile 145	Ala 145	Leu 145	Thr 150	Asp 150	Gly 150	Glu 150	Leu 155	His 155	Glu 155	Asp 155	Leu 160	Phe 160	Phe 160	Tyr 160
Ser 165	Glu 165	Arg 165	Glu 165	Ala 165	Asn 170	Arg 170	Ser 170	Arg 170	Asp 170	Leu 175	Gly 175	Ala 175	Ile 175	Val 175	Tyr 175
Cys 180	Val 180	Gly 180	Val 180	Lys 185	Asp 185	Phe 185	Asn 185	Glu 185	Thr 190	Gln 190	Leu 190	Ala 190	Arg 190	Ile 195	Ala 195
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Gln 215	Gly 215	Ile 215	Ile 215	His 220	Ser 220	Ile 220	Leu 225	Lys 225	Lys 225	Ser 230	Cys 230	Ile 230	Glu 235	Ile 235	Leu 235
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Ala 395	Leu 395	Leu 395	Trp 400	Trp 400	Phe 405	Trp 405	Pro 410	Leu 410	Cys 415	Cys 415	Thr 420	Val 420	Ile 425	Ile 425	Lys 425
Glu 430	Val 430	Pro 435	Pro 435	Pro 440	Pro 440	Ala 445	Glu 445	Glu 445	Ser 450	Glu 450	Glu 450	Glu 455	Asp 455	Asp 455	Asp 455
Gly 460	Leu 460	Pro 465	Lys 465	Lys 470	Lys 470	Trp 475	Pro 475	Thr 480	Val 480	Asp 485	Ala 485	Ser 490	Tyr 490	Tyr 490	Gly 490
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Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro	
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Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln	
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Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile	
135 140 145	
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Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu	
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Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser	
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Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly	
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Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala	
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Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg	
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Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser	
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Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ser Val	
260 265 270	

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 Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly
 275 280 285 290

 atg aaa gct gca ctc cag gtc agc atg aac gat ggc ctc tct ttt atc 1030
 Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile
 295 300 305

 tcc agt tct gtc atc atc acc acc aca cac tgt agc ctc cac aaa att 1078
 Ser Ser Ser Val Ile Ile Thr Thr His Cys Ser Leu His Lys Ile
 310 315 320

 gca tca ggc ccc aca aca gct gct tgc atg gaa tagcagagaa taccgcctgc 1131
 Ala Ser Gly Pro Thr Thr Ala Ala Cys Met Glu
 325 330

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<211> 333

<212> PRT

<213> Homo sapiens

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Ser	Leu	Ala	Thr	Leu	Val	Leu	Ile	Cys	Ala	Gly	Gln	Gly	Gly	Arg	Arg	20	25	30	
Glu	Asp	Gly	Gly	Pro	Ala	Cys	Tyr	Gly	Gly	Phe	Asp	Leu	Tyr	Phe	Ile	35	40	45	
Leu	Asp	Lys	Ser	Gly	Ser	Val	Leu	His	His	Trp	Asn	Glu	Ile	Tyr	Tyr	50	55	60	
Phe	Val	Glu	Gln	Leu	Ala	His	Lys	Phe	Ile	Ser	Pro	Gln	Leu	Arg	Met	65	70	75	80
Ser	Phe	Ile	Val	Phe	Ser	Thr	Arg	Gly	Thr	Thr	Leu	Met	Lys	Leu	Thr	85	90	95	
Glu	Asp	Arg	Glu	Gln	Ile	Arg	Gln	Gly	Leu	Glu	Glu	Leu	Gln	Lys	Val	100	105	110	
Leu	Pro	Gly	Gly	Asp	Thr	Tyr	Met	His	Glu	Gly	Phe	Glu	Arg	Ala	Ser	115	120	125	
Glu	Gln	Ile	Tyr	Tyr	Glu	Asn	Arg	Gln	Gly	Tyr	Arg	Thr	Ala	Ser	Val	130	135	140	
Ile	Ile	Ala	Leu	Thr	Asp	Gly	Glu	Leu	His	Glu	Asp	Leu	Phe	Phe	Tyr	145	150	155	160
Ser	Glu	Arg	Glu	Ala	Asn	Arg	Ser	Arg	Asp	Leu	Gly	Ala	Ile	Val	Tyr	165	170	175	
Cys	Val	Gly	Val	Lys	Asp	Phe	Asn	Glu	Thr	Gln	Leu	Ala	Arg	Ile	Ala	180	185	190	
Asp	Ser	Lys	Asp	His	Val	Phe	Pro	Val	Asn	Asp	Gly	Phe	Gln	Ala	Leu	195	200	205	
Gln	Gly	Ile	Ile	His	Ser	Ile	Leu	Lys	Lys	Ser	Cys	Ile	Glu	Ile	Leu	210	215	220	
Ala	Ala	Glu	Pro	Ser	Thr	Ile	Cys	Ala	Gly	Glu	Ser	Phe	Gln	Val	Val	225	230	235	240
Val	Arg	Gly	Asn	Gly	Phe	Arg	His	Ala	Arg	Asn	Val	Asp	Arg	Val	Leu	245	250	255	
Cys	Ser	Phe	Lys	Ile	Asn	Asp	Ser	Val	Thr	Leu	Asn	Glu	Lys	Pro	Phe	260	265	270	
Ser	Val	Glu	Asp	Thr	Tyr	Leu	Leu	Cys	Pro	Ala	Pro	Ile	Leu	Lys	Glu	275	280	285	
Val	Gly	Met	Lys	Ala	Ala	Leu	Gln	Val	Ser	Met	Asn	Asp	Gly	Leu	Ser	290	295	300	

Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Leu His
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Lys Ile Ala Ser Gly Pro Thr Thr Ala Ala Cys Met Glu
325 330

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Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr
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acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta 460
Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu
15 20 25
gaa gaa ctc cag aaa gtt ctg cca gga gga gac act tac atg cat gaa 508
Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu
30 35 40
gga ttt gaa agg gcc agt gag cag att tat tat gaa aac aga caa ggg 556
Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly
45 50 55
tac agg aca gct agc gtc atc att gct ttg act gat gga gaa ctc cat 604
Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His
60 65 70 75
gaa gat ctc ttt ttc tat tca gag agg gag gct aat agg tct cga gat 652
Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp
80 85 90
ctt ggt gca att gtt tac tgt gtt ggt gtg aaa gat ttc aat gag aca 700
Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr
95 100 105

cag ctg gcc cgg att gcg gac agt aag gat cat gtg ttt ccc gtg aat 748
 Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val Asn
 110 115 120

 gac ggc ttt cag gct ctg caa ggc atc atc cac tca att ttg aag aag 796
 Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys
 125 130 135

 tcc tgc atc gaa att cta gca gct gaa cca tcc acc ata tgt gca gga 844
 Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly
 140 145 150 155

 gag tca ttt caa gtt gtc gtg aga gga aac ggc ttc cga cat gcc cgc 892
 Glu Ser Phe Gln Val Val Val Arg Gly Asn Gly Phe Arg His Ala Arg
 160 165 170

 aac gtg gac agg gtc ctc tgc agc ttc aag atc aat gac tcg gtc aca 940
 Asn Val Asp Arg Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr
 175 180 185

 ctc agt aag tcc ttg cag agt cca tgg gtt tct tcg aca agt ggc ttc 988
 Leu Ser Lys Ser Leu Gln Ser Pro Trp Val Ser Ser Thr Ser Gly Phe
 190 195 200

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 Lys Glu Gly Asn Ser His Pro Cys Leu Pro Ala Arg Pro His Thr
 205 210 215

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 Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys
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